

seq_name: gb_ba2:AE000213

seq_documentation_block:

LOCUS AE000213 10959 bp DNA BCT 12-NOV-1998
DEFINITION Escherichia coli K-12 MG1655 section 103 of f the complete
genome.
ACCESSION AE000213 U00096
VERSION AE000213.1 GI:1787371
KEYWORDS
SOURCE Escherichia coli.

ORGANISM Escherichia coli

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.

REFERENCE 1 (bases 1 to 10959)

AUTHORS Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V.,
Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F.,
Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J.,
Mau, B. and Shao, Y.

TITLE The complete genome sequence of Escherichia coli K-12⁴

JOURNAL Science 277 (5331), 1453-1474 (1997)

MEDLINE 97426617

REFERENCE 2 (bases 1 to 10959)

AUTHORS Blattner, F.R.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecolie@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459

REFERENCE 3 (bases 1 to 10959)

AUTHORS Blattner, F.R.

TITLE Direct Submission

JOURNAL Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecolie@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459

REFERENCE 4 (bases 1 to 10959)

AUTHORS Plunkett, G. III.

TITLE Direct Submission

alignment_scores:

Quality: 983.60 Length: 218
Ratio: 4.795 Gaps: 0
Percent Similarity: 94.037 Percent Identity: 85.780

alignment_block:

US-09-252-691-7056 x AE000213/rev

Align seg 1/1 to reverse of: AE000213 from: 1 to: 10959

1 AlaIleMetArgGlnLeuIleThrProGluAsnThrMetThrLvsThrSa 17
|||||
268 GCTATAATGCGGCAATTCATAATCTCTGAAATACCATGCAAAACTTC 9219
17 rPheArgLysHisArgValGluArgPheSerSerArgGlnAlaThrArgA 34
|||||
9218 TTTTAGAAATCACCAGGTTAAGCGATTCAGCTCGCAACGTTCTACCAGGC 9169
34 rgThrProGluProGlnProThrArgValIleLeuPheAsnLysProTyr 50
|||||
9168 GTAAACCTGAAACACGACCCACGCGTGTGATCTGTTCATAAACCTAC 9119
51 AspValLeuProGlnPheThrAspGluAlaGlyArgSerThrLeuLysAs 67
|||||
9118 GATGTTCTTCCGAGTTCACCGATGAAGCCGACGCAAAACATTAAAGA 9069
67 pPheIleProValGlnGlyValTyrAlaAlaGlyArgLeuAspArgAspS 84
|||||
9068 ATTCATCCCGTTTCAAGGTGTTTATGCAGCAGGTCGCCTTGACCGCGATA 9019
84 erGluGlyLeuLeuValLeuThrAsnAspGlyValLeuGlnAlaArgLeu 100
|||||
9018 GCGAAGGTTGCTGGTGTGACCAATAACGGCGGTTGACGCGCGTTA 8969
101 ThrGlnProGlyLysArgThrGlyLysIleTyrTyrValGlnValGluG1 117
|||||
8968 ACCCAGCCGGGTAAACGACCGGAAAAATCTATTATGTGAGGTGGAAGG 8919
117 yGluProAspAspAlaSerLeuAlaLysLeuArgAsnGlyValThrLeuA 134
|||||
8918 TATTCACACACAAGACGCACTTGAAGCTTGCAGCAATGGCGTAACCTTAA 8869
134 snAspGlyProThrLeuProAlaGlyIleGluArgValAsnGluProGlu 150
|||||
8868 ATGATGGCCCTACCTGCCCCCGGCGCGGAGCTGGTTGACGAACCCGCG 8819
151 TrpLeuTrpProArgAsnProProIleArgGluArgLysSerIleProTh 167
|||||
8818 TGGTTATGGCCGCGGAATCCACCAATTCGTGAACGCAAAAGTATTCCAC 8769
167 rSerTrpLeuLysIleThrLeuTyrGluGlyArgAsnArgGlnValArgA 184
|||||
8768 CAGCTGGCTGAAGATCACCTTATATGAAGGACGTAATCGCCAGGTGCGCC 8719
184 rgMetThrAlaHisValGlyPheProThrLeuArgLeuIleArgTyrAla 200
|||||
8718 GCATGACCGCCATGTTGGCTTCCCCACGCTGCGACTGATTCGCTATGCG 8669
201 MetGlySerTyrThrLeuAspSerLeuAlaAsnGlyGluTrpArgAspVa 217
|||||
8668 ATGGGTGATTACTCTTTGGATAATCTTGCCAATGGTGAATGGCGAGAAGT 8619
217 lThr 218
|||||
8618 GACA 8615

ALIGNMENTS

RESULT 1
 YMFEC_ECOLI
 ID YMFEC_ECOLI STANDARD; PRT; 217 AA.
 AC P75966;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 24.9 KD PROTEIN IN TRMU-ICDA INTERGENIC REGION.
 GN YMFEC.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE: 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE: 97061202.
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Takemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map."
 RL DNA Res. 3:137-155 (1996).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF PSEUDOURIDINE SYNTHASES.
 CC STRONG, TO H.INFLUENZAE HI0694.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 DR EMBL; AE000213; AAC74219.1; ALT_INIT.
 DR EMBL; D90748; BAA35957.1; -.
 DR EMBL; D90749; BAA35966.1; -.
 DR EMBL; EGI3447; YMFEC.
 DR PROSITE; PS01149; PSI_RSU; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 217 AA; 24880 MW; F7C7A7CEDC5FD3F6 CRC64;

Query Match 83.7%; Score 975; DB 1; Length 217;
 Best Local Similarity 85.6%; Pred. No. 3.8e-79;

Matches 185; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 3 MRQLITPENTMTKTSFRKHRVERFSSRQATRRTPPEQPTRVILFNKPYDVLPOFTDEAGR 62
 Db 1 MRQFIISENTMQKTSFRNHQVKRFSSQRSTRKPEQPTRVILFNKPYDVLPOFTDEAGR 60
 QY 63 STLKDFIPVQGVYAAGRLDRDSEGLLVLTNDGVLOARLTQPGKRTGKIYYVQVEGEPDDA 122
 Db 61 KTLKEFIPVQGVYAAGRLDRDSEGLLVLTNNGALQARLTQPGKRTGKIYYVQVEGIPTQD 120
 QY 123 SLAKLRNGVTLNDGPTLPAGIERVNEPEWLWPRNPPIRERKSIPTSWLKITLYEGRNRQV 182
 Db 121 ALEALRNGVTLNDGPTLPAGAEVLVDEPAWLWPRNPPIRERKSIPTSWLKITLYEGRNRQV 180
 QY 183 RRMTAHVGFPTLRLIRYAMGSYTLDSLANGEWRDVT 218
 Db 181 RRMTAHVGFPTLRLIRYAMGDYSLDNLANGEWREVT 216

52

RESULT 10

W10941

ID W10941 standard; peptide; 35 AA.

AC W10941;

DT 10-NOV-1997 (first entry)

DE Polyclonal anti-ferritin binder sequence, C28, from R26 library.

KW Functional surrogate; analyte; affinity receptor; immunoreactive group;

KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;

KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;

KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;

KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;

KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;

KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;

KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;

KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

OS Synthetic.

PN W09641172-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; U10498.

PR 07-JUN-1995; US-476375.

PA (CYTO-) CYTOGEN CORP.

PI Carted JM, Lee-Own FV;

DR WPI; 97-077284/07.

DR N-PSDB; T48787.

PT Labelled functional surrogate of an analyte - useful as competitor

PT molecule in affinity assays, esp. for detecting large macromolecules

PT such as ferritin

PS Disclosure; Page 118/2; 156pp; English.

CC This sequence represents a polyclonal anti-ferritin binder sequence from

CC the R26 library (C series) which may be used in the conjugate of the

CC invention. The novel labelled conjugate comprises at least one label
CC attached to a functional surrogate of an analyte of interest. The
CC surrogate is capable of competing effectively with the analyte for a
CC limiting amount of an affinity receptor for the analyte. The conjugate
CC exhibits an activity that is altered upon interaction with the affinity
CC receptor and this activity can be measured and related to the amount of
CC the analyte present in a sample. Functional surrogates such as this have
CC an immunoreactive group that allows the surrogate to compete effectively
CC and with the analyte for a limiting amount of its affinity receptor.
CC Functional surrogates are able to mimic naturally occurring analytes.
CC They can be labelled for use in standard competitive affinity assays
CC (esp. homogenous immunoassays) for detecting large macromolecules such
CC as polypeptides, polysaccharides, polynucleotides, glycoproteins and
CC lipid-containing macromolecules, as well as small haptens. Typical
CC diagnostic analytes for detection include cardiac or tumour markers,
CC allergens, hormones related to fertility-pregnancy or analytes associated
CC with infectious disease. In particular, the assays are useful for
CC detecting ferritin, follicle stimulating hormone, human growth hormone,
CC immunoglobulin E, prolactin, parathyroid hormone, human placental
CC lactogen, hepatitis antigens or antibodies against them, human
CC chorionic gonadotropin, human luteinising hormone, cytomegalovirus,
CC Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB,
CC myoglobin, myosin light chain, troponin, carcinoembryonic antigen,
CC alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).

SQ Sequence 35 AA;

Query Match 2.7%; Score 6; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 AAGRLD 81
| | | | |
Db 17 AAGRLD 22